

## SEQUENCE LISTING

<110> Curtis, Rory A. J.  
 Silos-Santiago, Inmaculada

<120> 53010, A NOVEL HUMAN CARBOXYLESTERASE  
 FAMILY MEMBER AND USES THEREOF

<130> 10448-122001

<150> 60/256,369  
 <151> 2000-12-18

<150> 60/279,508  
 <151> 2001-03-28

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<170> FastSEQ for Windows Version 4.0

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 Met Pro Gln Gly Leu Thr  
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tca tct gct tca caa tgg tgc ttt ttc ctg att ctc cag ccc ctg ttg 161  
 Ser Ser Ala Ser Gln Trp Cys Phe Phe Leu Ile Leu Gln Pro Leu Leu  
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gga cac aga cag tgg gga aaa act ggg cct tct gct gaa ggg cca cag 209  
 Gly His Arg Gln Trp Gly Lys Thr Gly Pro Ser Ala Glu Gly Pro Gln  
 25 30 35

agg aac acc agg ctg gga tgg att cag ggc aag caa gtc act gtg ctg 257  
 Arg Asn Thr Arg Leu Gly Trp Ile Gln Gly Lys Gln Val Thr Val Leu  
 40 45 50

gga agc cct gtg cct gtg aac gtg ttc ctc gga gtc ccc ttt gct gct 305  
 Gly Ser Pro Val Pro Val Asn Val Phe Leu Gly Val Pro Phe Ala Ala  
 55 60 65 70

ccc ccg ctg gga tcc ctg cga ttt acg aac ccg cag cct gca tgg ccc 353  
 Pro Pro Leu Gly Ser Leu Arg Phe Thr Asn Pro Gln Pro Ala Ser Pro  
 75 80 85

tgg gat aac ttg cga gaa gcc acc tcc tac cct_aat ttg tgc ctc cag	401
Trp Asp Asn Leu Arg Glu Ala Thr Ser Tyr Pro Asn Leu Cys Leu Gln	
90 95 100	
aac tca gag tgg ctg ctc tta gat caa cac atg ctc aag gtg cat tac	449
Asn Ser Glu Trp Leu Leu Leu Asp Gln His Met Leu Lys Val His Tyr	
105 110 115	
ccg aaa ttc gga gtg tca gaa gac tgc ctc tac ctg aac atc tat gcg	497
Pro Lys Phe Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Ala	
120 125 130	
cct gcc cac gcc gat aca ggc tcc aag ctc ccc gtc ttg gtg tgg ttc	545
Pro Ala His Ala Asp Thr Gly Ser Lys Leu Pro Val Leu Val Trp Phe	
135 140 145 150	
cca gga ggt gcc ttc aag act ggc tca gcc tcc atc ttt gat ggg tcc	593
Pro Gly Gly Ala Phe Lys Thr Gly Ser Ala Ser Ile Phe Asp Gly Ser	
155 160 165	
gcc ctg gct gcc tat gag gac gtg ctg gtt gtg gtc gtc cag tac cgg	641
Ala Leu Ala Ala Tyr Glu Asp Val Leu Val Val Val Val Gln Tyr Arg	
170 175 180	
cta gga ata ttt ggt ttc ttc acc aca tgg gat cag cat gct ccg ggg	689
Leu Gly Ile Phe Gly Phe Phe Thr Thr Trp Asp Gln His Ala Pro Gly	
185 190 195	
aac tgg gcc ttc aag gac cag gtg gct gct ctg tcc tgg gtc cag aag	737
Asn Trp Ala Phe Lys Asp Gln Val Ala Ala Leu Ser Trp Val Gln Lys	
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aac atc gag ttc ttc ggt ggg gac ccc agc tct gtg acc atc ttt ggc	785
Asn Ile Glu Phe Phe Gly Gly Asp Pro Ser Ser Val Thr Ile Phe Gly	
215 220 225 230	
gag tcc gcg gga gcc ata agt gtt tct agt ctt ata ctg tct ccc atg	833
Glu Ser Ala Gly Ala Ile Ser Val Ser Ser Leu Ile Leu Ser Pro Met	
235 240 245	
gcc aaa ggc tta ttc cac aaa gcc atc atg gag agt ggg gtg gcc atc	881
Ala Lys Gly Leu Phe His Lys Ala Ile Met Glu Ser Gly Val Ala Ile	
250 255 260	
atc cct tac ctg gag gcc cat gat tat gag aag agt gag gac ctg cag	929
Ile Pro Tyr Leu Glu Ala His Asp Tyr Glu Lys Ser Glu Asp Leu Gln	
265 270 275	
gtg gtt gca cat ttc tgt ggt aac aat gcg tca gac tct gag gcc ctg	977
Val Val Ala His Phe Cys Gly Asn Asn Ala Ser Asp Ser Glu Ala Leu	
280 285 290	
ctg agg tgc ctg agg aca aaa ccc tcc aag gag ctg ctg acc ctc agc	1025
Leu Arg Cys Leu Arg Thr Lys Pro Ser Lys Glu Leu Leu Thr Leu Ser	
295 300 305 310	

cag aaa aca aag tct ttc act cga gtg gtt gat ggt gct ttc ttt cct Gln Lys Thr Lys Ser Phe Thr Arg Val Val Asp_Gly Ala Phe Phe Pro	1073
315 320 325	
aat gag cct cta gat cta ttg tct cag aaa gca ttt aaa gca att cct Asn Glu Pro Leu Asp Leu Ser Gln Lys Ala Phe Lys Ala Ile Pro	1121
330 335 340	
tcc atc atc gga gtc aat aac cac gag tgt ggc ttc ctg ctg cct atg Ser Ile Ile Gly Val Asn Asn His Glu Cys Gly Phe Leu Leu Pro Met	1169
345 350 355	
aag gag gct cct gag atc ctc agt ggc tcc aac aag tcc ctt gcc ctc Lys Glu Ala Pro Glu Ile Leu Ser Gly Ser Asn Lys Ser Leu Ala Leu	1217
360 365 370	
cat ctg ata caa aac atc ctg cac atc ccg cct cag tat ttg cac ctt His Leu Ile Gln Asn Ile Leu His Ile Pro Pro Gln Tyr Leu His Leu	1265
375 380 385 390	
gtg gct aat gaa tac ttc cat gac aag cac tcc ctg act gaa atc cga Val Ala Asn Glu Tyr Phe His Asp Lys His Ser Leu Thr Glu Ile Arg	1313
395 400 405	
gac agt ctt ctg gac ttg ctt gga gat gtg ttc ttt gtg gtc cct gca Asp Ser Leu Leu Asp Leu Leu Gly Asp Val Phe Phe Val Val Pro Ala	1361
410 415 420	
ctg atc aca gct cga tat cac aga gat gct ggt gca cct gtc tac ttc Leu Ile Thr Ala Arg Tyr His Arg Asp Ala Gly Ala Pro Val Tyr Phe	1409
425 430 435	
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440 445 450	
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455 460 465 470	
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475 480 485	
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cga acc ggg aat cct aat ggg aac gac ctg tct ctg tgg cca gct tat Arg Thr Gly Asn Pro Asn Gly Asn Asp Leu Ser Leu Trp Pro Ala Tyr	1649
505 510 515	
aat ctg act gag cag tac ctc cag ctg gac ttg aac atg agc ctc gga Asn Leu Thr Glu Gln Tyr Leu Gln Leu Asp Leu Asn Met Ser Leu Gly	1697
520 525 530	
cag aga ctc aaa gaa ccg cgg gtg gat ttt tgg acc agc acc atc ccc	1745

Gln Arg Leu Lys Glu Pro Arg Val Asp Phe Trp Thr Ser Thr Ile Pro	
535 540 545 550	
ctg atc ctg tct gcc tcc gac atg ctc cac agf cct ctt tct tcc tta	1793
Leu Ile Leu Ser Ala Ser Asp Met Leu His Ser Pro Leu Ser Ser Leu	
555 560 565	
act ttc ctc tct ctc ctc cag cct ttc ttt ttc ttt tgt gct cct	1838
Thr Phe Leu Ser Leu Leu Gln Pro Phe Phe Phe Phe Cys Ala Pro	
570 575 580	
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cattagcttc tttctgagct cagctgcttt ctatggggat ccttgcaaaa caagctgctt	1958
tcgctgatat tttatggact taggaatgat ccttacagaa tctctttcaa catcaaaaag	2018
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 <212> PRT  
 <213> Homo sapiens

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Ser Ala Glu Gly Pro Gln Arg Asn Thr Arg Leu Gly Trp Ile Gln Gly	
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Lys Gln Val Thr Val Leu Gly Ser Pro Val Pro Val Asn Val Phe Leu	
50 55 60	
Gly Val Pro Phe Ala Ala Pro Pro Leu Gly Ser Leu Arg Phe Thr Asn	
65 70 75 80	
Pro Gln Pro Ala Ser Pro Trp Asp Asn Leu Arg Glu Ala Thr Ser Tyr	
85 90 95	
Pro Asn Leu Cys Leu Gln Asn Ser Glu Trp Leu Leu Leu Asp Gln His	
100 105 110	
Met Leu Lys Val His Tyr Pro Lys Phe Gly Val Ser Glu Asp Cys Leu	
115 120 125	
Tyr Leu Asn Ile Tyr Ala Pro Ala His Ala Asp Thr Gly Ser Lys Leu	
130 135 140	
Pro Val Leu Val Trp Phe Pro Gly Gly Ala Phe Lys Thr Gly Ser Ala	
145 150 155 160	
Ser Ile Phe Asp Gly Ser Ala Leu Ala Ala Tyr Glu Asp Val Leu Val	
165 170 175	
Val Val Val Gln Tyr Arg Leu Gly Ile Phe Gly Phe Phe Thr Thr Trp	
180 185 190	
Asp Gln His Ala Pro Gly Asn Trp Ala Phe Lys Asp Gln Val Ala Ala	
195 200 205	
Leu Ser Trp Val Gln Lys Asn Ile Glu Phe Phe Gly Gly Asp Pro Ser	
210 215 220	
Ser Val Thr Ile Phe Gly Glu Ser Ala Gly Ala Ile Ser Val Ser Ser	
225 230 235 240	
Leu Ile Leu Ser Pro Met Ala Lys Gly Leu Phe His Lys Ala Ile Met	
245 250 255	
Glu Ser Gly Val Ala Ile Ile Pro Tyr Leu Glu Ala His Asp Tyr Glu	

260 265 270  
 Lys Ser Glu Asp Leu Gln Val Val Ala His Phe\_Cys Gly Asn Asn Ala  
 275 280 285  
 Ser Asp Ser Glu Ala Leu Leu Arg Cys Leu Arg Thr Lys Pro Ser Lys  
 290 295 300  
 Glu Leu Leu Thr Leu Ser Gln Lys Thr Lys Ser Phe Thr Arg Val Val  
 305 310 315 320  
 Asp Gly Ala Phe Phe Pro Asn Glu Pro Leu Asp Leu Leu Ser Gln Lys  
 325 330 335  
 Ala Phe Lys Ala Ile Pro Ser Ile Ile Gly Val Asn Asn His Glu Cys  
 340 345 350  
 Gly Phe Leu Leu Pro Met Lys Glu Ala Pro Glu Ile Leu Ser Gly Ser  
 355 360 365  
 Asn Lys Ser Leu Ala Leu His Leu Ile Gln Asn Ile Leu His Ile Pro  
 370 375 380  
 Pro Gln Tyr Leu His Leu Val Ala Asn Glu Tyr Phe His Asp Lys His  
 385 390 395 400  
 Ser Leu Thr Glu Ile Arg Asp Ser Leu Leu Asp Leu Leu Gly Asp Val  
 405 410 415  
 Phe Phe Val Val Pro Ala Leu Ile Thr Ala Arg Tyr His Arg Asp Ala  
 420 425 430  
 Gly Ala Pro Val Tyr Phe Tyr Glu Phe Arg His Arg Pro Gln Cys Phe  
 435 440 445  
 Glu Asp Thr Lys Pro Ala Phe Val Lys Ala Asp His Ala Asp Glu Val  
 450 455 460  
 Arg Phe Val Phe Gly Ala Phe Leu Lys Gly Asp Ile Val Met Phe  
 465 470 475 480  
 Glu Gly Ala Thr Glu Glu Lys Leu Leu Ser Arg Lys Met Met Lys  
 485 490 495  
 Tyr Trp Ala Thr Phe Ala Arg Thr Gly Asn Pro Asn Gly Asn Asp Leu  
 500 505 510  
 Ser Leu Trp Pro Ala Tyr Asn Leu Thr Glu Gln Tyr Leu Gln Leu Asp  
 515 520 525  
 Leu Asn Met Ser Leu Gly Gln Arg Leu Lys Glu Pro Arg Val Asp Phe  
 530 535 540  
 Trp Thr Ser Thr Ile Pro Leu Ile Leu Ser Ala Ser Asp Met Leu His  
 545 550 555 560  
 Ser Pro Leu Ser Ser Leu Thr Phe Leu Ser Leu Leu Gln Pro Phe Phe  
 565 570 575  
 Phe Phe Cys Ala Pro  
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&lt;210&gt; 3

&lt;211&gt; 1746

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

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ccgcagcctg	catgccctcg	ggataacttg	cgagaagcca	cctcctaccc	taatttgtgc	300
ctccagaact	cagagtggct	gctcttagat	caacacatgc	tcaaggtgca	ttaccggaaa	360
ttcggagtgt	cagaagactg	cctctacctg	aacatctatg	cgcttgccca	cgccgataca	420
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gccatcatcc pttacotgga ggcccatgat tatgagaaga gtgaggacct gcaggtgggt 840
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cgggtggatt tttggaccag caccatcccc ctgatctgt ctgcctccga catgctccac 1680
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<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence

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35 40 45
Leu Asp Ala Thr Lys Tyr Pro Pro Ser Cys Leu Gln Asp Asp Asp Phe
50 55 60
Gly Phe Ser Leu Ser Asp Leu Lys Val Ala Leu Lys Met Leu Ser Leu
65 70 75 80
Gly Trp Asn Lys Leu Val Gly Leu Lys Leu Ser Glu Asp Cys Leu Tyr
85 90 95
Leu Asn Val Tyr Thr Pro Lys Asn Thr Lys Pro Asn Ser Lys Leu Pro
100 105 110
Val Met Val Trp Ile His Gly Gly Gly Phe Met Phe Gly Ser Gly His
115 120 125
Ser Leu Pro Leu Ser Leu Tyr Asp Gly Glu Ser Leu Ala Arg Glu Gly
130 135 140
Asn Val Ile Val Val Ser Ile Asn Tyr Arg Leu Gly Pro Leu Gly Phe
145 150 155 160
Leu Ser Thr Gly Asp Asp Lys Leu Pro Gly Ser Gly Asn Tyr Gly Leu
165 170 175
Leu Asp Gln Arg Leu Ala Leu Lys Trp Val Gln Asp Asn Ile Ala Ala
180 185 190
Phe Gly Gly Asp Pro Asn Ser Val Thr Ile Phe Gly Glu Ser Ala Gly
195 200 205

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Ala Ala Ser Val Ser Leu Leu Leu Ser Asn Gly Gly Asp Asn Pro
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Pro Ser Ser Lys Gly Leu Phe His Arg Ala Ile Ser Gln Ser Gly Ser
225 230 235 240
Ala Leu Ser Pro Trp Ala Ile Gln Ser Glu Ser Asn Ala Arg Gly Arg
245 250 255
Ala Lys Glu Leu Ala Arg Leu Leu Gly Cys Asn Glu Thr Ser Ser Ser
260 265 270
Glu Leu Leu Asp Cys Leu Arg Ser Lys Ser Ala Glu Glu Leu Leu Glu
275 280 285
Ala Thr Arg Ser Phe Leu Leu Phe Glu Tyr Val Pro Phe Leu Pro Leu
290 295 300
Phe Leu Ala Phe Gly Pro Val Val Asp Gly Asp Ala Pro Glu Ala
305 310 315 320
Phe Ile Pro Glu Asp Pro Glu Glu Leu Ile Lys Glu Gly Lys Phe Ala
325 330 335
Asp Val Pro Tyr Leu Ile Gly Val Thr Lys Asp Glu Gly Tyr Phe
340 345 350
Ala Ala Met Leu Leu Asn Ala Ser Ser Lys Gly Glu Asp Glu Leu Lys
355 360 365
Lys Glu Thr Asn Pro Asp Val Trp Leu Glu Leu Lys Tyr Leu Leu
370 375 380
Phe Tyr Ala Ser Glu Ala Leu Asn Ile Lys Asp Met Asp Asp Leu Ala
385 390 395 400
Asp Lys Val Leu Glu Lys Tyr Pro Gly Asp Val Asp Asp Phe Ser Val
405 410 415
Glu Ser Arg Lys Pro Asn Leu Gln Asp Met Leu Thr Asp Leu Leu Phe
420 425 430
Lys Cys Pro Thr Arg Val Ala Ala Asp Leu His Ala Lys His Gly Gly
435 440 445
Ser Pro Val Tyr Ala Tyr Val Phe Asp His Pro Ala Ser Phe Gly Ile
450 455 460
Gly Gln Phe Leu Ala Lys Arg Val Asp Pro Glu Phe Gly Gly Ala Val
465 470 475 480
His Gly Asp Glu Ile Phe Phe Val Phe Gly Asn Pro Leu Leu Lys Glu
485 490 495
Gln Leu Tyr Lys Ala Thr Glu Glu Glu Lys Ser Ser Ser Lys Thr
500 505 510
Met Met Asn Tyr Trp Ala Asn Phe Ala Lys Thr Gly Asn Pro Asn Asn
515 520 525
Gly Thr Ser Asn Gly Leu Val Val Trp Pro Lys Tyr Thr Ser Glu Glu
530 535 540
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<210> 5

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary motif

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 <223> Xaa = Any amino acid  
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 <223> Xaa = Leu, Ile, Val, or Met  
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 <223> Xaa = Leu, Ile, or Val  
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 <223> Xaa = Ser, Thr, Ala, or Gly  
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 Phe Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Ser Xaa Gly  
 1 5 10 15  
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 <221> VARIANT  
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 <223> Xaa = Tyr, or Thr  
 <221> VARIANT  
 <222> 6, 8  
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 <222> 9  
 <223> Xaa = Leu, Ile, Val, Phe, Tyr, or Trp  
 <221> VARIANT  
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 <223> Xaa = Any amino acid  
 <221> VARIANT  
 <222> (0)...(11)  
 <223> Xaa = Pro, Gln, or Arg



&lt;400&gt; 6

Xaa Asp Cys Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1

5

10

9

4

1

9